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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/297,181

DATE: 09/14/1999
TIME: 12:27:59

Input Set: I297181.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1  <110> APPLICANT: Bracco, Laurent
2      Debussche, Laurent
3  <120> TITLE OF INVENTION: ANTI-P53 SINGLE-CHAIN ANTIBODY FRAGMENTS AND THEIR USES
4  <130> FILE REFERENCE: ST96030-US
5  <140> CURRENT APPLICATION NUMBER: US/09/297,181
6  <141> CURRENT FILING DATE: 1999-04-26
7  <150> EARLIER APPLICATION NUMBER: PCT/FR97/01921
8  <151> EARLIER FILING DATE: 1997-10-27
9  <150> EARLIER APPLICATION NUMBER: FR96/13176
10 <151> EARLIER FILING DATE: 1996-10-29
11 <160> NUMBER OF SEQ ID NOS: 4
12 <170> SOFTWARE: PatentIn Ver. 2.0
13 <210> SEQ ID NO 1
14 <211> LENGTH: 729
15 <212> TYPE: DNA
16 <213> ORGANISM: Mus musculus
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18 <221> NAME/KEY: CDS
19 <222> LOCATION: (1)..(729)
20 <400> SEQUENCE: 1
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23      1              5              10              15
24      tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac tac      96
25      Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Tyr
26      20              25              30
27      tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att      144
28      Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
29      35              40              45
30      gga tgg att gat cct gag aat ggt gat act gaa tat gcc ccg aag ttc      192
31      Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
32      50              55              60
33      cag ggc aag gcc act atg act gca gac aca tcc tcc aat aca gcc tac      240
34      Gln Gly Lys Ala Thr Met Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
35      65              70              75              80
36      ctg cag ctc agc agc ctg gca tct gag gac act gcc gtc tat tat tgt      288
37      Leu Gln Leu Ser Ser Leu Ala Ser Glu Asp Thr Ala Val Tyr Tyr Cys
38      85              90              95
39      aat ttt tac ggg gat gct ttg gac tat tgg ggc caa ggg acc acg gtc      336
40      Asn Phe Tyr Gly Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
41      100             105             110
42      acc gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt      384
43      Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
44      115             120             125

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45      ggc gga tcg gat gtt ttg atg acc caa act cca ctc act ttg tcg gtt      432
46      Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro Leu Thr Leu Ser Val
47      130                                135                                140
48      acc att gga caa cca gcc tcc atc tct tgc aag tca agt cag agc ctc      480
49      Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
50      145                                150                                155                                160
51      ttg gat agt gat gga aag aca tat ttg aat tgg ttg tta cag agg cca      528
52      Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
53      165                                170                                175
54      ggc cag tct cca aag cgc cta atc tat ctg gtg tct aaa ctg gac tct      576
55      Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
56      180                                185                                190
57      gga gtc cct gac agg ttc act ggc agt gga tca ggg aca gat ttc aca      624
58      Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
59      195                                200                                205
60      ctg aaa atc aac aga gtg gag gct gag gat ttg gga gtt tat tat tgc      672
61      Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
62      210                                215                                220
63      tgg caa ggt aca cat tct ccg ctc acg ttc ggt gct ggc acc aag ctg      720
64      Trp Gln Gly Thr His Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
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67      Glu Ile Lys
68      <210> SEQ ID NO 2
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76      20                                25                                30
77      Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
78      35                                40                                45
79      Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
80      50                                55                                60
81      Gln Gly Lys Ala Thr Met Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
82      65                                70                                75                                80
83      Leu Gln Leu Ser Ser Leu Ala Ser Glu Asp Thr Ala Val Tyr Tyr Cys
84      85                                90                                95
85      Asn Phe Tyr Gly Asp Ala Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
86      100                                105                                110
87      Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
88      115                                120                                125
89      Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro Leu Thr Leu Ser Val
90      130                                135                                140
91      Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
92      145                                150                                155                                160
93      Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
94      165                                170                                175

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95      Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
96              180              185              190
97      Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
98              195              200              205
99      Leu Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
100             210             215             220
101      Trp Gln Gly Thr His Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
102             225             230             235             240
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106      <212> TYPE: DNA
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108      <220> FEATURE:
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110      <222> LOCATION: (1)..(747)
111      <400> SEQUENCE: 3
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114             1             5             10             15
115      tca gtc aat ttg tcc tgc aca gct tct ggc ttc aac att aaa gac tac      96
116      Ser Val Asn Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Tyr
117             20             25             30
118      tat atg cac tgg gtg aaa cag agg cct gaa gag ggc ctg gag tgg att      144
119      Tyr Met His Trp Val Lys Gln Arg Pro Glu Glu Gly Leu Glu Trp Ile
120             35             40             45
121      gga tat att gat cct gag agt ggt gaa act gaa tat gcc ccg aac ttc      192
122      Gly Tyr Ile Asp Pro Glu Ser Gly Glu Thr Glu Tyr Ala Pro Asn Phe
123             50             55             60
124      cag ggc aag gcc act gtg act gca gac aca tcc tcc aac aca gcc tac      240
125      Gln Gly Lys Ala Thr Val Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
126             65             70             75             80
127      ctg cac ctc agc agc ctg aca tct gag gac aca acc gtc tat tac tgt      288
128      Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Thr Val Tyr Tyr Cys
129             85             90             95
130      aat gca gtc atc tac tat gaa tac gac ggc tat gct ttg gac tac tgg      336
131      Asn Ala Val Ile Tyr Tyr Glu Tyr Asp Gly Tyr Ala Leu Asp Tyr Trp
132             100            105            110
133      ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc      384
134      Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
135             115            120            125
136      gga ggt ggc tct ggc ggt ggc gga tcg gac att gag ctc acc cag tct      432
137      Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
138             130            135            140
139      cca tct tcc ctg gct gtg tca gca gga gag aag gtc gct atg agc tgc      480
140      Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Ala Met Ser Cys
141             145            150            155            160
142      aaa tcc agt cag agt ctg ttc aac agt aga acc cga aag aat tac ttg      528
143      Lys Ser Ser Gln Ser Leu Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu
144             165            170            175

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145      gct tgg tat cag cag aaa cca ggg cag tct cct aaa gtg ctg atc tac      576
146      Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr
147              180                      185                      190
148      tgg gca tcc act agg gaa tct gga gtc cct gat cgc ttc aca ggc agt      624
149      Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser
150              195                      200                      205
151      gga tct ggg aca gat ttc act ctc acc atc agc agt gtg cag gct gaa      672
152      Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu
153              210                      215                      220
154      gac ctg gca gtt tat tac tgc aag caa tct tat aat cta ccg acg ttc      720
155      Asp Leu Ala Val Tyr Tyr Cys Lys Gln Ser Tyr Asn Leu Pro Thr Phe
156      225                      230                      235                      240
157      ggc ggg ggc acc aag ctg gaa atc aaa      747
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163      <213> ORGANISM: Mus musculus
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168              20              25              30
169      Tyr Met His Trp Val Lys Gln Arg Pro Glu Glu Gly Leu Glu Trp Ile
170              35              40              45
171      Gly Tyr Ile Asp Pro Glu Ser Gly Glu Thr Glu Tyr Ala Pro Asn Phe
172              50              55              60
173      Gln Gly Lys Ala Thr Val Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
174              65              70              75              80
175      Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Thr Val Tyr Tyr Cys
176              85              90              95
177      Asn Ala Val Ile Tyr Tyr Glu Tyr Asp Gly Tyr Ala Leu Asp Tyr Trp
178              100             105             110
179      Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
180              115             120             125
181      Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser
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183      Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Lys Val Ala Met Ser Cys
184      145             150             155             160
185      Lys Ser Ser Gln Ser Leu Phe Asn Ser Arg Thr Arg Lys Asn Tyr Leu
186              165             170             175
187      Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr
188              180             185             190
189      Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser
190              195             200             205
191      Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu
192              210             215             220
193      Asp Leu Ala Val Tyr Tyr Cys Lys Gln Ser Tyr Asn Leu Pro Thr Phe
194      225             230             235             240

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195	Gly Gly Gly Thr Lys Leu Glu Ile Lys
196	245

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
